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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
08/973,363	02/04/1998	RICHARD GRIFFITHS	263PPNTIR117	6817

7590 06/04/2003

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EXAMINER
SCHNIZER, RICHARD A

ART UNIT	PAPER NUMBER
1635	32

DATE MAILED: 06/04/2003

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No. 08/973,363	Applicant(s) Griffiths
	Examiner Richard Schnizer	Art Unit 1635

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136 (a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
- Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1) ☒ Responsive to communication(s) filed on *Mar 17, 2003*.

2a) ☐ This action is **FINAL**. 2b) ☒ This action is non-final.

3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11; 453 O.G. 213.

Disposition of Claims

4) ☒ Claim(s) *34, 36, 40, 42, 44, 46, 48, 49, and 55-60* is/are pending in the application.

4a) Of the above, claim(s) _____ is/are withdrawn from consideration.

5) ☒ Claim(s) *34* is/are allowed.

6) ☒ Claim(s) *36, 40, 42, 44, 46, 48, 49, and 55-60* is/are rejected.

7) ☐ Claim(s) _____ is/are objected to.

8) ☐ Claims _____ are subject to restriction and/or election requirement.

Application Papers

9) ☒ The specification is objected to by the Examiner.

10) ☒ The drawing(s) filed on *Feb 4, 1998* is/are a) ☐ accepted or b) ☒ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

11) ☐ The proposed drawing correction filed on _____ is: a) ☐ approved b) ☐ disapproved by the Examiner.

If approved, corrected drawings are required in reply to this Office action.

12) ☐ The oath or declaration is objected to by the Examiner.

Priority under 35 U.S.C. §§ 119 and 120

13) ☒ Acknowledgement is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a) ☒ All b) ☐ Some* c) ☐ None of:

1. ☒ Certified copies of the priority documents have been received.
2. ☐ Certified copies of the priority documents have been received in Application No. _____.
3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

*See the attached detailed Office action for a list of the certified copies not received.

14) ☐ Acknowledgement is made of a claim for domestic priority under 35 U.S.C. § 119(e).

a) ☐ The translation of the foreign language provisional application has been received.

15) ☐ Acknowledgement is made of a claim for domestic priority under 35 U.S.C. §§ 120 and/or 121.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO-1449) Paper No(s). _____
4) ☐ Interview Summary (PTO-413) Paper No(s). _____
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other:

[redacted]

DETAILED ACTION

An amendment was received and entered as Paper No. 31 on 3/17/03.

Claims 35, 37-39, 41, 43, 45, 47, and 50-54 were canceled and claims 57-60 were added as requested.

Claims 34, 36, 40, 42, 44, 46, 48, 49, and 55-60 are pending and under consideration in this Office Action.

Claims 55 and 56 were previously found to be allowable. This finding is withdrawn in view of the new grounds of rejection set forth below. In view of the new grounds of rejection, this Office Action is NON-FINAL.

Rejections Withdrawn

The rejection of claims 34, 36, 40, 42, 44, 46, 48, 49 under 35 USC 112, second paragraph is withdrawn in view of Applicant's amendments.

The rejection of claims 36, 40, 42, 44, and 46 under 35 USC 102 over Delmas is withdrawn in view of Applicant's amendment.

Compliance with Sequence Rules

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825 for the

[redacted]

following reason(s). Applicant's attention is directed to the final rule making notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998). Nucleic acid sequences in excess of 9 nucleotides are disclosed in the specification at page 18, lines 12-14 and page 19, lines 23 and 24, but these sequences are not identified by any SEQ ID NO. An amino sequences in excess of three amino acids are disclosed at page 32, lines 25 and 26, but these sequences are not identified by any SEQ ID NO. Originally filed Figs 1, 3, 5, 7-11 and 14 also disclose nucleic acid or amino acid sequences which are not identified by SEQ ID NOS. **EVERY INSTANCE OF A NUCLEOTIDE SEQUENCE LONGER THAN 9 RESIDUES, AND EVERY INSTANCE OF AN AMINO ACID SEQUENCE LONGER THAN 4 RESIDUES, MUST BE IDENTIFIED BY A SEQ ID NO.** It is not sufficient to identify these sequences in only a single passage of the specification. For example, Applicant has amended the specification at pages 4, 8, 14, and 27 to reflect that certain figures disclose certain SEQ ID NOS. However, if a Figure discloses a SEQ ID NO, then the SEQ ID NO must be recited in either the Figure itself, or in the brief description of the Figure. Similarly, the oligonucleotides disclosed at page 18 of specification must be identified by SEQ ID NOS at that passage in the specification.

Applicant is advised that the amendments to pages 4, 8, and 27 in some cases fail to unambiguously define which SEQ ID NO corresponds to which sequence. For example, at page 8 the specification as amended indicates that SEQ ID NOS: 2-9 are contained in Fig. 3, but fails to

tell which SEQ ID NOS in Fig.3 correspond to which sequences. It is also noted that Applicant submitted Figures in Paper No. 6, filed March 9, 1998, but because these Figures were not accompanied by any amendment directed their entry into the specification, the original Figures have not been replaced. Also, Fig. 3 lists 153 bases of sequence from each of four different genes, wherein the 153 bases are set forth in three segments of 50, 50, and 53 bases, respectively. The Schedule for Sequence Listing submitted 3/9/98 and identifies the first 50 bases of each sequence by a SEQ ID NO, but fails to identify the remaining sequences by any SEQ ID NO. Analysis of the sequences listed for CHD-1A shows that the 153 bases in Fig. 3 are not contiguous within the sequence of CHD-1A, therefore Fig. 3 appears to disclose 12 distinct nucleic acid sequences, 8 of which are not identified by SEQ ID NO. Finally, it is not clear that the current CRF lists the amino acid sequences on page 32 described above.

Although Applicant submitted a paper copy of the Sequence Listing in Paper No. 31, this copy was not accompanied by a statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d). As such, even if the Sequence Listing does contain all of the sequences disclosed in the specification, and it is not clear that it contains the amino acid sequences at page 32, lines 25 and 26, the paper copy of the Sequence Listing would be insufficient because it was not accompanied by the statement set forth above.

[redacted]

If the sequence listing does not reflect the amino acid sequences at page 32, lines 25 and 26, then Applicant must provide:

A substitute computer readable form (CRF) copy of the "Sequence Listing".

An substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

If the Sequence Listing does contain all of the sequences disclosed in the specification, Applicant must still provide a statement indicating that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

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Specification

The specification is objected to because of an apparent typographical error at page 29, line 22. In view of Figure 17, and the specification at page 29, line 17, the numeral "3" should be substituted for the numeral "13" at page 29, line 22.

Claim Objections

Claims 48 and 49 are objected to as ungrammatical. The second instance of the word "to" in step (ii) of the claims should be changed to the word "than".

Double Patenting

A rejection based on double patenting of the "same invention" type finds its support in the language of 35 U.S.C. 101 which states that "whoever invents or discovers any new and useful process ... may obtain a patent therefor ..." (Emphasis added). Thus, the term "same invention," in this context, means an invention drawn to identical subject matter. See *Miller v. Eagle Mfg. Co.*, 151 U.S. 186 (1894); *In re Ockert*, 245 F.2d 467, 114 USPQ 330 (CCPA 1957); and *In re Vogel*, 422 F.2d 438, 164 USPQ 619 (CCPA 1970).

A statutory type (35 U.S.C. 101) double patenting rejection can be overcome by canceling or amending the conflicting claims so they are no longer coextensive in scope. The filing of a terminal disclaimer cannot overcome a double patenting rejection based upon 35 U.S.C. 101.

[redacted]

Applicant is advised that should claim 34 be found allowable, claim 55 will be objected to under 37 CFR 1.75 as being a substantial duplicate thereof. When two claims in an application are duplicates or else are so close in content that they both cover the same thing, despite a slight difference in wording, it is proper after allowing one claim to object to the other as being a substantial duplicate of the allowed claim. See MPEP § 706.03(k). In this case, claims 1 and 55 are both drawn to isolated polynucleotides consisting of the nucleotide sequence set forth in SEQ ID NO: 1, 3, 4, 5, 10, 12, 13, or 15. The only difference between claims 34 and 55 is the claim 34 also requires that the polynucleotides must be isolated from a CH-D gene of a bird, and must be hybridizable to the genomic DNA of a bird. Claim 34 additionally requires that the polynucleotides must be isolated from a CH-D gene of a bird. This product by process language is given no weight in determining patentability in the instant case, because the physical attributes of each polynucleotide are fully described in its sequence (SEQ ID). Similarly the functional language requiring hybridization fails to distinguish the claims because the physical attributes of each polynucleotide are fully described by the SEQ ID NO.

Claim Rejections - 35 USC § 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

[redacted]

Written Description

Claims 36, 40, 42, 44, 46, 48, 49, and 56-59 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

Claims 36, 40, 44, and 46 are drawn to the genus of fragments of SEQ ID NOS: 1, 3, 4, 5, 10, 12, 13, or 15 that give a specific signal only on the W chromosome upon hybridization to restriction endonuclease-digested non-ratite bird genomic DNA.

It is apparent from the specification that non-ratite birds contain a W-linked CHD-W gene, and a closely related autosomal CHD-1A gene. SEQ ID NOS: 3, 10, and 12 correspond to the chicken CHD-1A autosomal locus. SEQ ID NOS: 4, 13, and 15 correspond to the chicken W-linked CHD-W locus. SEQ ID NOS: 1 and 5 correspond to the great tit CHD-W locus. A comparison of W-linked SEQ ID NOS: 4, 5, and 13 to the CHD-1A autosomal locus shows that these sequences are 95%, 90%, and 93% identical over their entire lengths to segments of the autosomal CHD-1A locus. So, even under the high stringency hybridization conditions disclosed in the specification that require 90% identity for binding, each of these sequences would bind to autosomal CHD-1A sequences. For this reason, none of these sequences could provide a specific signal only on the W chromosome, as required by the claims. The specification fails to teach any other sequence capable of binding only to a W chromosome sequence and not an autosomal sequence. Because the specification fails to teach a single sequence that hybridizes only to W

chromosome sequences, one of skill in the art could not conclude that Applicant was in possession of the claimed invention at the time the invention was filed.

These claims also require knowledge of what restriction endonucleases will digest CHD-A and CHD-1A DNAs such that the products are distinguishable, as do claims 48, 49 and 57-59. This would require foreknowledge of the complete restriction maps of CHD-1A and CHD-W loci of all non-ratite birds. The specification teaches that HaeIII digestion yields a W-specific banding pattern in four species of birds, and that DdeI should work as well for chicken and Spix's Macaw. See page 28 and 29. However, the specification notes that there is no reason to believe that these sites will be conserved across all non-ratite bird species, but fails to teach any restriction enzyme that will work for all birds. For this reason, one of skill in the art cold not conclude that Applicant was in possession of the knowledge of which restriction enzymes will provide W-specific restriction patterns for the entire genus of non-ratite birds at the time the invention was filed.

Claims 42, 44, and 46 are drawn to the genus of polynucleotides that hybridize under high stringency conditions to SEQ ID NOS: 1, 3, 5, 10, 12, 13, or 15. In analyzing whether the written description requirement is met for genus claims, it is first determined whether a representative number of species has been described by complete structure, such as nucleotide sequence, next it is determined whether a representative number of species has been described by other relevant identifying characteristics, such as by functional characteristics coupled with a known or disclosed correlation between structure and function. The specification exemplifies

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high stringency conditions at page 9, lines 8-16, and notes that these conditions correspond with about 90% sequence identity. The specification discloses that none of SEQ ID NOS: 1, 3, 5, 10, 12, 13, or 15 corresponds to a complete open reading frame, as each of these sequences is either a partial cDNA or partial genomic clone. For this reason, claim 42 reads on cDNAs and genomic clones that are more complete than SEQ ID NOS: 1, 3, 5, 10, 12, 13, or 15, i.e. sequences that are 10% longer than SEQ ID NOS: 1, 3, 5, 10, 12, 13, or 15. The specification fails to describe a single species of such sequences, and fails to establish any correlation between structure and function. For this reason one of skill in the art could not conclude that Applicant was in possession of the claimed invention at the time the invention was filed.

Claim 56 is drawn to the genus of isolated polynucleotides consisting of a sequence that encodes a polypeptide having the amino acid sequence of SEQ ID NOS: 6-9, 11, or 14.

These claims read on full length cDNAs and genomic clones encoding any bird CHD gene. Polynucleotides encoding the amino acid sequence of SEQ ID NO:6 were known in the prior art (Delmas et al (1993) of record). SEQ ID NOS: 7-9, 11, and 14 correspond to avian CHD polypeptides encoded by partial cDNAs. The specification discloses various genomic and cDNA fragments of CHD genes from the mouse and from two birds, but fails to disclose any full-length cDNA of any avian CHD gene, any full-length genomic clone of any avian CHD gene, any common sequence which is shared by all the members of the claimed genus, nor any sequence characteristic which identifies any sequence as having been derived from a bird rather than from some other animal. The specification indicates that all birds are believed to have two or more

CHD type genes, one W-linked, and one either autosomal or Z-linked. See page 4, lines 1-8. Because the specification discloses sequences from only two birds, but all birds are expected to have CHD-genes, the claimed genus is considered to embrace an enormous number of sequences which have yet to be discovered. Because the disclosed sequences do not include any full-length genomic or cDNA clones, and include no sequence identified as common to all the members of the genus, the disclosed sequences do not constitute a substantial portion of the claimed genus.

Weighing the available evidence, i.e. the lack of disclosure of full-length cDNA or genomic clones, the breadth of the claims which clearly encompasses such sequences from any bird, and the failure to identify any sequence common to all of the members of the genus, one of skill in the art could not conclude that Applicant was in possession of the claimed genus at the time of filing.

Claims 57-59 are drawn to the genus of primer oligonucleotides that amplify a product from any avian CHD-W gene that is distinguishable by its size from any product amplified from a CHD-1A gene, thereby allowing sex determination of birds by PCR. The specification exemplifies a single set of nested PCR primers for sex identification of birds. These primers were used to amplify nucleic acids three species of birds. See Fig. 17. The products were all of the same length, therefore the PCR products generated from CHD-1A and CHD-W templates were of the same length, and are only distinguishable by restriction digest or sequencing. In fact, the specification teaches that it is a criterion for PCR-based sex determination that the PCR products can be separated by restriction digestion. See page 28, lines 26 and 27. The specification fails to

[redacted]

teach a single example of PCR primer pairs that can be used to amplify CHD-W products of a different size than the those obtained from the endogenous CHD-1A template, and explicitly states that restriction digestion is necessary to resolve the products. Thus one of skill in the art could not conclude that Applicant was in possession of the claimed invention at the time the invention was filed.

Enablement

Claims 36, 40, 44, 46, 48, 49 and 56-58 are rejected under 35 U.S.C. 112, first paragraph, because the specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention commensurate in scope with these claims.

Claims 36, 40, 44, 46, and 48 are drawn to fragments of SEQ ID NOS: 1, 3, 4, 5, 10, 12, 13, or 15 that give a specific signal only on the W chromosome upon hybridization to restriction endonuclease-digested non-ratite bird genomic DNA.

As discussed above under written description, it is apparent from the specification that non-ratite birds contain a W-linked CHD-W gene, and a closely related autosomal CHD-1A gene. SEQ ID NOS: 3, 10, and 12 correspond to the chicken CHD-1A autosomal locus. SEQ ID NOS: 4, 13, and 15 correspond to the chicken W-linked CHD-W locus. SEQ ID NOS: 1 and 5 correspond to the great tit CHD-W locus. A comparison of W-linked SEQ ID NOS: 4, 5, and 13 to the CHD-1A autosomal locus shows that these sequences are 95%, 90%, and 93% identical

over their entire lengths to segments of the autosomal CHD-1A locus. So, even under the high stringency hybridization conditions disclosed in the specification that require 90% identity for binding, each of these sequences would bind to autosomal CHD-1A sequences. For this reason, none of these sequences could provide a specific signal only on the W chromosome, as required by the claims. The specification fails to teach any other sequence capable of binding only to a W chromosome sequence and not an autosomal sequence. While Applicant is not required to disclose that which is well known in the art, there is an obligation to disclose critical elements of the invention as well as how to use these elements. In Genentech, Inc, v Novo Nordisk A/S, the court found that when the specification omits any specific starting material required to practice an invention, or the conditions under which a process can be carried out, there is a failure to meet the enablement requirement. See 42 USPQ2d 1001.

> It is true, as Genentech argues, that a specification need not disclose what is well known in the art. See, e.g., Hybritech Inc. v. Monoclonal Antibodies, Inc., 802 F.2d 1367, 1385, 231 USPQ 81, 94 (Fed. Cir. 1986). However, that general, oft-repeated statement is merely a rule of supplementation, not a substitute for a basic enabling disclosure. It means that the omission of minor details does not cause a specification to fail to meet the enablement requirement. However, when there is no disclosure of any specific starting material or of any of the conditions under which a process can be carried out, undue experimentation is required; there is a failure to meet the enablement requirement that cannot be rectified by asserting that all the disclosure related to the process is within the skill of the art. It is the specification, not the knowledge of one skilled in the art, that must supply the novel aspects of an invention in order to constitute adequate enablement. This specification provides only a starting point, a direction for further research.

In this case, the identification of polynucleotides that give a specific signal only on the W chromosome upon hybridization to restriction endonuclease-digested non-ratite bird genomic DNA is a critical element of the invention, cannot be considered a minor detail which can be omitted in the process of providing an enabling disclosure. Because the specification fails to teach

any polynucleotides that give a specific signal only on the W chromosome upon hybridization to restriction endonuclease-digested non-ratite bird genomic DNA, one of skill in the art would have to perform undue experimentation in order to practice the invention as claimed.

With regard to claims 48 and 57-59, the specification is enabling for embodiments of the claimed methods that depend on restriction digestion for discriminating between CHD-W and CHD-1A DNAs, but fails to reasonably enable methods that require either 1) restriction digestion of RNAs, or 2) discriminating between CHD-W and CHD-1A PCR products by size alone without any restriction digestion step.

The claimed invention embraces methods wherein RNAs from cells or tissue of a non-ratite bird, fetus or embryo are subject to restriction endonuclease digestion, the results of which are diagnostic of the sex of the organism. A search of the prior art failed to reveal any restriction endonucleases that can cleave RNAs, and the specification fails to teach any. Given that the art fails to teach restriction endonuclease digestion of RNAs, and the specification fails to provide the guidance that is missing from the prior art, one of skill in the art would have to perform undue experimentation in order to practice the claimed invention commensurate in scope with its breadth.

As discussed above under written description, claims 57-59 are drawn methods of using primer oligonucleotides to amplify a product from a CHD-W gene that is distinguishable by its size from any product amplified from a CHD-1A gene. The claims embrace an embodiment wherein PCR products are subjected to a diagnostic restriction digest. This embodiment is

enabled. The specification also embraces methods that do not allow for diagnostic restriction digestion, but which require the simultaneous generation of different sized PCR products from CHD-W and CHD-1A templates using the same primers. The specification fails to teach any primer set that achieves this result, and the evidence of record indicates that it is not possible. The specification discloses a single set of nested PCR primers and shows that PCR products amplified from three species of birds all gave rise to only a single length product, therefore the PCR products generated from CHD-1A and CHD-W templates were of identical length. In fact, the specification teaches that it is a criterion for PCR-based sex determination that the PCR products should be separable by restriction digestion. See page 28, lines 26 and 27. Because the specification does not teach any example of PCR primer pairs that can be used to amplify different sized CHD-W and CHD-1A products, and explicitly states that restriction digestion is necessary to resolve the products, one of skill in the art would have to perform undue experimentation in order to practice the claimed invention commensurate in scope with its breadth.

Claims 48, 49, and 57-59 also lack enablement because they lack an essential method step in which the DNA restriction fragments from females are compared to those from males. In the absence of forknowledge regarding the precise restriction banding pattern obtained from digestion of CHD-W DNA, one would have to rely on a comparison between similarly treated DNAs from males and females in order to establish the expected pattern for CHD-1A and discriminate the pattern for CHD-W. The specification fails to provide sufficient guidance for one of skill in the art to practice the claimed methods without this comparison step.

Claim 49 is also not enabled because it lacks further essential method steps and materials. In step (i), the claim requires hybridization of DNA or RNA of a non-ratite bird, but it fails to disclose with what the DNA or RNA should be hybridized. The claim then requires in step (ii) restriction endonuclease digestion of the hybrids from step (i). A search of the prior art failed to reveal any restriction endonucleases that can cleave duplex RNAs or RNA/DNA/hybrids that would be produced by step (i), and the specification fails to teach any. Because the claim fails to teach a critical method step, i.e. the selection of an agent to hybridize to the DNA or RNA in steps (i)(a)-(i)(c), and because polynucleotide the specification fails to provide the guidance that is missing from the prior art regarding restriction endonucleases capable of digesting RNAs or RNA/DNA hybrids, one of skill in the art would have to perform undue experimentation in order to practice the claimed invention commensurate in scope with its breadth.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless -
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Claims 56 is rejected under 35 U.S.C. 102(b) as being anticipated by Delmas et al (1998).

Claim 56 embraces an isolated polynucleotide consisting of a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence of SEQ ID NO:6. Delmas teaches an

isolated polynucleotide that encodes a mouse CHD-1 polypeptide. The polypeptide comprises residues 1286-1326 which are identical to SEQ ID NO:6. See Fig.1 at page 2425 of Delmas.

Thus Delmas anticipates the claims.

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

Claim 60 is rejected under 35 U.S.C. 103(a) as being unpatentable over Funahasi et al (GenBank Accession No. D14316, published 8/5/1993).

Claim 60 embraces an isolated polynucleotide consisting of the sequence of SEQ ID NO:39, i.e. ATATTCTTGATCTGATAGTGATC, or ATATTCTTGATCTGATAGTGACT. Funahasi teaches a nucleotide sequence encoding a polypeptide that binds to the delta crystallin enhancer. The open reading frame encoding the polypeptide extends from positions 257-1939, and when fused to beta galactosidase binds to blocks 10-3 of the delta crystallin enhancer. The nucleic acid sequence comprises the sequence ATATTCTTGATCTGATAGTGACT at positions 1282-1304. See alignment below.

[redacted]

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   >gi|391639|dbj|D14316.1|   Gallus gallus mRNA for delta-
crystallin enhancer binding protein,
           complete CDs
         Length = 2292

 Score = 46.1 bits (23), Expect = 6e-04
 Identities = 23/23 (100%)
 Strand = Plus / Plus


Query: 1    atattctggatctgatagtgact 23
            |||||||||||||||||||||||
Sbjct: 1282 atattctggatctgatagtgact 1304
```

It would have been obvious to one of ordinary skill in the art to select as an upstream PCR primer any sequence within the sequence of Funahasi, including one consisting of SEQ ID NO:39, in order to amplify a segment of the open reading frame for further analysis. One would have been motivated to do so in order to determine what fraction of the encoded protein is sufficient to allow binding to the enhancer sequence.

Thus the invention as a whole was prima facie obvious.

Response to Arguments

Applicant's arguments filed 3/17/03 have been fully considered but they are not persuasive.

At page 7 of the response Applicant argues that the rejection of claims 34-49 for lack of adequate written description should be overcome by replacing the term "comprising" in claim 44

with :consisting of". This argument is persuasive, but a new ground of rejection, not addressed by Applicant's arguments, is set forth above.

At pages 7 and 8 of the response, Applicant addresses the enablement rejection, indicating that amendment of claims 36, 44, 48, and 49 to require restriction digestion should overcome the rejection. This argument is persuasive with regard to claims 36, 40, 44, and 46, but a new ground of rejection, not addressed by Applicant's arguments, is set forth above. The argument is not fully persuasive with respect to claim 48, because this claim embraces methods of digesting RNAs with restriction endonucleases. The Examiner is unaware of any restriction endonuclease that is active on an RNA, there is no art of record indicating the existence of such a restriction endonuclease, and Applicant has presented no evidence or argument to the contrary, so the rejection of claim 48 is maintained.

Conclusion

Claim 34 is allowable. Claims 36, 40, 42, 44, 46, 48, 49, 55, and 57-59 are free of the art of record.

Any inquiry concerning this communication or earlier communications from the examiner(s) should be directed to Richard Schnizer, whose telephone number is 703-306-5441. The examiner can normally be reached Monday through Friday between the hours of 6:20 AM and 3:50 PM. The examiner is off on alternate Fridays, but is sometimes in the office anyway.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, John Leguyader, can be reached at 703-308-0447. The FAX numbers for art unit 1632 are 703-308-4242, and 703-305-3014. Additionally correspondence can be transmitted to the following RIGHTFAX numbers: 703-872-9306 for correspondence before final rejection, and 703-872-9307 for correspondence after final rejection.

Inquiries of a general nature or relating to the status of the application should be directed to the Patent Analyst Trina Turner whose telephone number is 703-305-3413.

Richard Schnizer, Ph.D.

DAVE T. NGUYEN
PRIMARY EXAMINER

[redacted]